PCT10

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,228A

DATE: 07/17/2002
TIME: 09:11:24

Input Set : A:\EP.txt
Output Set: N:\CRF3\07172002\J018228A.raw

```
       5  <110> APPLICANT: Lex M. Cowsert
       6        ISIS PHARMACEUTICALS, INC.
       8  <120> TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-S1 EXPRESSION
W-->   9  <130> FILE REFERENCE: RTSP-0061
C-->  11  <140> CURRENT APPLICATION NUMBER: US/10/018,228A
C-->  11  <141> CURRENT FILING DATE: 2002-06-03
      11  <150> PRIOR APPLICATION NUMBER: 09/344,914
      12  <151> PRIOR FILING DATE: 1999-06-25
      14  <160> NUMBER OF SEQ ID NOS: 87
      16  <210> SEQ ID NO: 1
      17  <211> LENGTH: 1516
      18  <212> TYPE: DNA
      19  <213> ORGANISM: Homo sapiens
      21  <220> FEATURE:
      22  <221> NAME/KEY: CDS
      23  <222> LOCATION: (13)..(1155)
      25  <400> SEQUENCE: 1
      26     gccgccgccg cc atg ggc tgc ctc ggg aac agt aag acc gag gac cag          48
      27                   Met Gly Cys Leu Gly Asn Ser Lys Thr Glu Asp Gln
      28                    1               5                  10
      30     cgc aac gag gag aag gcg cag cgt gag gcc aac aaa aag atc gag aag          96
      31     Arg Asn Glu Glu Lys Ala Gln Arg Glu Ala Asn Lys Lys Ile Glu Lys
      32             15                  20                  25
      34     cag ctg cag aag gac aag cag gtc tac cgg gcc acg cac cgc ctg ctg         144
      35     Gln Leu Gln Lys Asp Lys Gln Val Tyr Arg Ala Thr His Arg Leu Leu
      36          30                  35                  40
      38     ctg ctg ggt gct gga gaa tct ggt aaa agc acc att gtg aag cag atg         192
      39     Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met
      40          45                  50                  55                  60
      42     agg atc ctg cat gtt aat ggg ttt aat gga gac agt gag aag gca acc         240
      43     Arg Ile Leu His Val Asn Gly Phe Asn Gly Asp Ser Glu Lys Ala Thr
      44                  65                  70                  75
      46     aaa gtg cag gac atc aaa aac aac ctg aaa gag gcg att gaa acc att         288
      47     Lys Val Gln Asp Ile Lys Asn Asn Leu Lys Glu Ala Ile Glu Thr Ile
      48                  80                  85                  90
      50     gtg gcc gcc atg agc aac ctg gtg ccc ccc gtg gag ctg gcc aac ccc         336
      51     Val Ala Ala Met Ser Asn Leu Val Pro Pro Val Glu Leu Ala Asn Pro
      52             95                 100                 105
      54     gag aac cag ttc aga gtg gac tac atc ctg agt gtg atg aac gtg cct         384
      55     Glu Asn Gln Phe Arg Val Asp Tyr Ile Leu Ser Val Met Asn Val Pro
      56            110                 115                 120
      58     gac ttt gac ttc cct ccc gaa ttc tat gag cat gcc aag gct ctg tgg         432
      59     Asp Phe Asp Phe Pro Pro Glu Phe Tyr Glu His Ala Lys Ala Leu Trp
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```
 60     125                   130                   135                   140
 62     gag gat gaa gga gtg cgt gcc tgc tac gaa cgc tcc aac gag tac cag      480
 63     Glu Asp Glu Gly Val Arg Ala Cys Tyr Glu Arg Ser Asn Glu Tyr Gln
 64                         145                   150                   155
 66     ctg att gac tgt gcc cag tac ttc ctg gac aag atc gac gtg atc aag      528
 67     Leu Ile Asp Cys Ala Gln Tyr Phe Leu Asp Lys Ile Asp Val Ile Lys
 68                         160                   165                   170
 70     cag gct gac tat gtg ccg agc gat cag gac ctg ctt cgc tgc cgt gtc      576
 71     Gln Ala Asp Tyr Val Pro Ser Asp Gln Asp Leu Leu Arg Cys Arg Val
 72                         175                   180                   185
 74     ctg act tct gga atc ttt gag acc aag ttc cag gtg gac aaa gtc aac      624
 75     Leu Thr Ser Gly Ile Phe Glu Thr Lys Phe Gln Val Asp Lys Val Asn
 76                   190                   195                   200
 78     ttc cac atg ttt gac gtg ggt ggc cag cgc gat gaa cgc cgc aag tgg      672
 79     Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp
 80     205                   210                   215                   220
 82     atc cag tgc ttc aac gat gtg act gcc atc atc ttc gtg gtg gcc agc      720
 83     Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Ile Phe Val Val Ala Ser
 84                         225                   230          ·        235
 86     agc agc tac aac atg gtc atc cgg gag gac aac cag acc aac cgc ctg      768
 87     Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Gln Thr Asn Arg Leu
 88                   240                   245                   250
 90     cag gag gct ctg aac ctc ttc aag agc atc tgg aac aac aga tgg ctg      816
 91     Gln Glu Ala Leu Asn Leu Phe Lys Ser Ile Trp Asn Asn Arg Trp Leu
 92                   255                   260                   265
 94     cgc acc atc tct gtg atc ctg ttc ctc aac aag caa gat ctg ctc gct      864
 95     Arg Thr Ile Ser Val Ile Leu Phe Leu Asn Lys Gln Asp Leu Leu Ala
 96             270                   275                   280
 98     gag aaa gtc ctt gct ggg aaa tcg aag att gag gac tac ttt cca gaa      912
 99     Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu
100     285                   290                   295                   300
102      ttt gct cgc tac act act cct gag gat gct act ccc gag ccc gga gag      960
103     Phe Ala Arg Tyr Thr Thr Pro Glu Asp Ala Thr Pro Glu Pro Gly Glu
104                         305                   310                   315
106     gac cca cgc gtg acc cgg gcc aag tac ttc att cga gat gag ttt ctg     1008
107     Asp Pro Arg Val Thr Arg Ala Lys Tyr Phe Ile Arg Asp Glu Phe Leu
108                   320                   325                   330
110     agg atc agc act gcc agt gga gat ggg cgt cac tac tgc tac cct cat     1056
111     Arg Ile Ser Thr Ala Ser Gly Asp Gly Arg His Tyr Cys Tyr Pro His
112             335                   340                   345
114     ttc acc tgc gct gtg gac act gag aac atc cgc cgt gtg ttc aac gac     1104
115     Phe Thr Cys Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe Asn Asp
116             350                   355                   360
118     tgc cgt gac atc att cag cgc atg cac ctt cgt cag tac gag ctg ctc     1152
119     Cys Arg Asp Ile Ile Gln Arg Met His Leu Arg Gln Tyr Glu Leu Leu
120     365                   370                   375                   380
122     taa gaagggaacc cccaaattta attaaagcct taagcacaat taattaaaag          1205
124     tgaaacgtaa ttgtacaagc agttaatcac ccaccatagg gcatgattaa caaagcaacc   1265
126     tttcccttcc cccgagtgat tttgcgaaac ccccttttcc cttcagcttg cttagatgtt   1325
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128    ccaaatttag aaagcttaag gcggcctaca gaaaaaggaa aaaaggccac aaaagttccc    1385
130    tctcactttc agtaaaaata aataaaacag cagcagcaaa caaataaaat gaaataaaag    1445
132    aaacaaatga aataaatatt gtgttgtgca gcattaaaaa aaatcaaaat aaaaattaaa    1505
134    tgtgagcaaa g                                                        1516
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 21
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: PCR Primer
144 <400> SEQUENCE: 2
145    cagtggagat gggcgtcact a                                              21
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 21
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: PCR Primer
155 <400> SEQUENCE: 3
156    atgtcacggc agtcgttgaa c                                              21
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 25
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: PCR Probe
166 <400> SEQUENCE: 4
167    tgctaccctc atttcacctg cgctg                                          25
169 <210> SEQ ID NO: 5
170 <211> LENGTH: 19
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: PCR Primer
177 <400> SEQUENCE: 5
178    gaaggtgaag gtcggagtc                                                 19
180 <210> SEQ ID NO: 6
181 <211> LENGTH: 20
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: PCR Primer
188 <400> SEQUENCE: 6
189    gaagatggtg atgggatttc                                                20
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 20
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
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197 <223> OTHER INFORMATION: PCR Probe
199 <400> SEQUENCE: 7
200    caagcttccc gttctcagcc                                        20
202 <210> SEQ ID NO: 8
203 <211> LENGTH: 20
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Antisense Oligonucleotide
210 <400> SEQUENCE: 8
211    tgccttctca ctgtctccat                                        20
213 <210> SEQ ID NO: 9
214 <211> LENGTH: 20
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Antisense Oligonucleotide
221 <400> SEQUENCE: 9
222    ttgccttctc actgtctcca                                        20
225 <210> SEQ ID NO: 10
226 <211> LENGTH: 20
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Antisense Oligonucleotide
233 <400> SEQUENCE: 10
234    gttgccttct cactgtctcc                                        20
236 <210> SEQ ID NO: 11
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Antisense Oligonucleotide
244 <400> SEQUENCE: 11
245    ggttgccttc tcactgtctc                                        20
247 <210> SEQ ID NO: 12
248 <211> LENGTH: 20
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Antisense Oligonucleotide
255 <400> SEQUENCE: 12
256    tggttgcctt ctcactgtct                                        20
258 <210> SEQ ID NO: 13
259 <211> LENGTH: 20
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Antisense Oligonucleotide

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Input Set : **A:\EP.txt**
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266 <400> SEQUENCE: 13
267    ctttggttgc cttctcactg                                    20
269 <210> SEQ ID NO: 14
270 <211> LENGTH: 20
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Antisense Oligonucleotide
277 <400> SEQUENCE: 14
278    gtgaaatgag ggtagcagta                                    20
280 <210> SEQ ID NO: 15
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Antisense Oligonucleotide
288 <400> SEQUENCE: 15
289    aggtgaaatg agggtagcag                                    20
291 <210> SEQ ID NO: 16
292 <211> LENGTH: 20
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Antisense Oligonucleotide
299 <400> SEQUENCE: 16
300    caggtgaaat gagggtagca                                    20
302 <210> SEQ ID NO: 17
303 <211> LENGTH: 20
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Antisense Oligonucleotide
310 <400> SEQUENCE: 17
311    gcaggtgaaa tgagggtagc                                    20
313 <210> SEQ ID NO: 18
314 <211> LENGTH: 20
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Antisense Oligonucleotide
321 <400> SEQUENCE: 18
322    cgcaggtgaa atgagggtag                                    20
324 <210> SEQ ID NO: 19
325 <211> LENGTH: 20
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Antisense Oligonucleotide
332 <400> SEQUENCE: 19
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**VERIFICATION SUMMARY**                    DATE: 07/17/2002
PATENT APPLICATION:   **US/10/018,228A**        TIME: 09:11:25

Input Set  : **A:\EP.txt**
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L:9 M:283 W: Missing Blank Line separator, <130> field identifier
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date